SEQUENCE LISTING

<110> Bayer HealthCare AG

<120>   Diagnostics and Therapeutics for Diseases Associated with N-
Acetylated Alpha-Linked Acidic Dipeptidase 2 (NAALADASE 2)

<130> BHC 03 01 004

<160> 5

<170> PatentIn version 3.1

<210> 1
<211> 3152
<212> DNA
<213> Homo sapiens

<400> 1
gctcgcgaat gtagcaggcg ccccaagctc ggtcctcaag aagccatggc ggaatccagg   60
ggccgtctgt acctttggat gtgcttggct gctgcgctgg catctttcct gatgggattt   120
atggtgggct ggtttattaa gcctctcaaa gaaacaacca cttctgtgcg ctatcatcaa   180
agtatacggt ggaaactggt atccgaaatg aaagctgaaa acatcaaatc atttcttcgt   240
tcttttacaa agcttcctca tctggcagga acagaacaaa atttcttgct tgccaagaaa   300
atccaaaccc agtggaagaa atttggacta gattcagcca agttggttca ttatgatgtc   360
ctcttatctt accccaatga gacaaatgcc aactatatat cgattgtgga tgaacatgaa   420
actgagattt tcaaaacatc ataccttgaa ccaccaccag atggctatga gaatgttaca   480
aatattgtgc caccatataa tgctttctca gcccaaggca tgccagaggg agatcttgta   540
tatgtgaact atgctcgcac tgaagacttt ttcaaactag aaagagagat gggcatcaac   600
tgtactggga agattgttat tgcaagatat ggaaaaatct tcagaggaaa taaagttaaa   660
aatgccatgt tagcaggagc cataggaatc atcttgtact cagatccagc tgactacttt   720
gctcctgagg tacagccata tcccaaagga tggaatcttc ctggaactgc agcccagaga   780
ggaaatgtgt taaatttgaa tggtgctggt gacccactca ctccaggcta ccagcaaaaa   840
gaatacactt tcagacttga tgttgaagaa ggagtgggaa tcccccgaat acctgtacat   900
cccattggat ataatgatgc agaaatatta ttacgctact gggaggaat tgctccacca   960
gataagagtt ggaagggagc ccttaatgtg agttatagta tcggacctgg ctttacaggg   1020
agtgattctt tcaggaaggt tagaatgcat gtttataaca tcaataaaat tacaaggatt   1080
tacaatgtag ttggaactat cagaggatct gtggaacctg acaggtatgt tattctggga   1140
ggtcaccggg actcctgggt atttggagct attgacccaa ccagtggggt tgctgttttg   1200
caagaaattg cccggagttt tggaaaactg atgagtaaag ctggagacc tagaagaact   1260
atcatttttg ccagctggga tgcagaagaa tttggacttc tgggttccac agaatgggct   1320
gaggagaatg tcaaaatact ccaggagaga agcattgctt atatcaactc ggattcatct   1380
atagaaggca attatactct cagagttgac tgtactcccc ttctttacca attagtgtat   1440
aaactgacaa aagagatccc cagccctgat gatgggtttg agagtaaatc actgtatgaa   1500
agctggttgg aaaaagaccc ttcacctgaa aataaaaatt gcctagaat caataagctg   1560

```
      ggatctggaa gtgactttga agcttatttt cagagacttg gaattgcttc aggcagagcc   1620
      cgttcacta agaataagaa aacagataag tacagcagct acccagtgta ccacacaatt   1680
      tatgagacat ttgaattggt agagaaattt tatgacccca catttaaaaa acaactttct   1740
      gtggctcaat tacgaggagc actggtatat gagcttgtgg attctaaaat cattcctttt   1800
      aatattcaag actatgcaga agctttgaaa aactatgcag caagtatcta taatctatct   1860
      aagaaacatg atcaacaatt aacagaccat ggagtatcat ttgactcctt attttctgct   1920
      gtgaaaaact tctcagaggc tgcttcgat tttcataaac gacttataca agttgatctt   1980
      aacaatccca ttgcagtgag aatgatgaat gaccaactga tgctcctgga aagagcattc   2040
      atcgatcctc ttggtttacc aggaaagctg ttctataggc acatcatatt tgctccaagt   2100
      agccacaaca aatatgctgg agaatcattt cctggaatct atgatgctat ctttgatatt   2160
      gaaaataaag ccaactctcg tttggcctgg aaagaagtaa agaaacatat ttctattgca   2220
      gcttttacaa ttcaagcagc agcaggaact ctgaaagaag tattatagaa ggtctcaagt   2280
      ggctagccat taaaggtgtt gctaaaagtc tgaggataaa attcaccttt ctgataactt   2340
      atgaagccag ggtgttctaa actcttttca tgtcatgttt tgattatagg ctttggtctt   2400
      ttcatctgca aagccttttt ttttttttgct ctttaaaagt taataattat attagcaaag   2460
      tgttaatcta atgaagtaaa aaactcctgt gtggcagaaa gtaaaagaaa attccctaaa   2520
      ttatagcaag gaacatgaat tctcagacat tgtgagtgtg ggaatgtaaa atggtaaaat   2580
      cacttttgaa aacagtttgg cagtttccta taaagttaaa catacacttt tactttagga   2640
      ctccagaatt ccacttctag ttatttattc aagagaagga aaaacaatga tcacagcaat   2700
      acttgtatgc atgttcattg caacttaaaa gcgtaaaaac cccaaatgtc catccacaga   2760
      cgaatgtata aactgtggta tccattacac aatagactac ttactactca gcaataaaaa   2820
      tgaagtaact ttcaataaat gcaatattat tggcagacat tgttgaagga aaaaagccag   2880
      acaaacaact acataaaata tgtttctatt tagatgaagt ggcaaactaa tctgtagtgt   2940
      taaaaattag attagtgatt gcctgggcca agtggcaggt tggggaggat ggctgcaaag   3000
      aagtatgagg aaacttttctc caatagatga gaattttccg tatcttgatc tgagtggcaa   3060
      attgtaaact taaaatatat ataaaattta ttgaaagaaa attaagcctc aataaacgtg   3120
      attataaaaa aaaaaaaaaa aagggcggcc gc   3152
```

```
<210>  2
<211>  740
<212>  PRT
<213>  Homo sapiens


<400>  2
Met Ala Glu Ser Arg Gly Arg Leu Tyr Leu Trp Met Cys Leu Ala Ala
1               5                   10                  15
Ala Leu Ala Ser Phe Leu Met Gly Phe Met Val Gly Trp Phe Ile Lys
                20                  25                  30
Pro Leu Lys Glu Thr Thr Thr Ser Val Arg Tyr His Gln Ser Ile Arg
            35                  40                  45
Trp Lys Leu Val Ser Glu Met Lys Ala Glu Asn Ile Lys Ser Phe Leu
        50                  55                  60
Arg Ser Phe Thr Lys Leu Pro His Leu Ala Gly Thr Glu Gln Asn Phe
65                  70                  75                  80
Leu Leu Ala Lys Lys Ile Gln Thr Gln Trp Lys Lys Phe Gly Leu Asp
```

```
                              85                    90                    95
        Ser Ala Lys Leu Val His Tyr Asp Val Leu Leu Ser Tyr Pro Asn Glu
                         100                   105                   110
        Thr Asn Ala Asn Tyr Ile Ser Ile Val Asp Glu His Glu Thr Glu Ile
  5                      115                   120                   125
        Phe Lys Thr Ser Tyr Leu Glu Pro Pro Pro Asp Gly Tyr Glu Asn Val
                     130                   135                   140
        Thr Asn Ile Val Pro Pro Tyr Asn Ala Phe Ser Ala Gln Gly Met Pro
        145                   150                   155                   160
 10     Glu Gly Asp Leu Val Tyr Val Asn Tyr Ala Arg Thr Glu Asp Phe Phe
                         165                   170                   175
        Lys Leu Glu Arg Glu Met Gly Ile Asn Cys Thr Gly Lys Ile Val Ile
                     180                   185                   190
        Ala Arg Tyr Gly Lys Ile Phe Arg Gly Asn Lys Val Lys Asn Ala Met
 15                  195                   200                   205
        Leu Ala Gly Ala Ile Gly Ile Ile Leu Tyr Ser Asp Pro Ala Asp Tyr
                     210                   215                   220
        Phe Ala Pro Glu Val Gln Pro Tyr Pro Lys Gly Trp Asn Leu Pro Gly
        225                   230                   235                   240
 20     Thr Ala Ala Gln Arg Gly Asn Val Leu Asn Leu Asn Gly Ala Gly Asp
                         245                   250                   255
        Pro Leu Thr Pro Gly Tyr Pro Ala Lys Glu Tyr Thr Phe Arg Leu Asp
                     260                   265                   270
        Val Glu Glu Gly Val Gly Ile Pro Arg Ile Pro Val His Pro Ile Gly
 25                  275                   280                   285
        Tyr Asn Asp Ala Glu Ile Leu Leu Arg Tyr Leu Gly Gly Ile Ala Pro
                 290                   295                   300
        Pro Asp Lys Ser Trp Lys Gly Ala Leu Asn Val Ser Tyr Ser Ile Gly
        305                   310                   315                   320
 30     Pro Gly Phe Thr Gly Ser Asp Ser Phe Arg Lys Val Arg Met His Val
                         325                   330                   335
        Tyr Asn Ile Asn Lys Ile Thr Arg Ile Tyr Asn Val Val Gly Thr Ile
                     340                   345                   350
        Arg Gly Ser Val Glu Pro Asp Arg Tyr Val Ile Leu Gly Gly His Arg
 35                  355                   360                   365
        Asp Ser Trp Val Phe Gly Ala Ile Asp Pro Thr Ser Gly Val Ala Val
                 370                   375                   380
        Leu Gln Glu Ile Ala Arg Ser Phe Gly Lys Leu Met Ser Lys Gly Trp
        385                   390                   395                   400
 40     Arg Pro Arg Arg Thr Ile Ile Phe Ala Ser Trp Asp Ala Glu Glu Phe
                         405                   410                   415
        Gly Leu Leu Gly Ser Thr Glu Trp Ala Glu Glu Asn Val Lys Ile Leu
                     420                   425                   430
        Gln Glu Arg Ser Ile Ala Tyr Ile Asn Ser Asp Ser Ser Ile Glu Gly
 45              435                   440                   445
```

```
        Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Leu Tyr Gln Leu Val
            450                 455                 460

        Tyr Lys Leu Thr Lys Glu Ile Pro Ser Pro Asp Asp Gly Phe Glu Ser
        465                 470                 475                 480

5       Lys Ser Leu Tyr Glu Ser Trp Leu Glu Lys Asp Pro Ser Pro Glu Asn
                        485                 490                 495

        Lys Asn Leu Pro Arg Ile Asn Lys Leu Gly Ser Gly Ser Asp Phe Glu
                    500                 505                 510

        Ala Tyr Phe Gln Arg Leu Gly Ile Ala Ser Gly Arg Ala Arg Tyr Thr
10              515                 520                 525

        Lys Asn Lys Lys Thr Asp Lys Tyr Ser Ser Tyr Pro Val Tyr His Thr
            530                 535                 540

        Ile Tyr Glu Thr Phe Glu Leu Val Glu Lys Phe Tyr Asp Pro Thr Phe
        545                 550                 555                 560

15      Lys Lys Gln Leu Ser Val Ala Gln Leu Arg Gly Ala Leu Val Tyr Glu
                        565                 570                 575

        Leu Val Asp Ser Lys Ile Ile Pro Phe Asn Ile Gln Asp Tyr Ala Glu
                    580                 585                 590

        Ala Leu Lys Asn Tyr Ala Ala Ser Ile Tyr Asn Leu Ser Lys Lys His
20              595                 600                 605

        Asp Gln Gln Leu Thr Asp His Gly Val Ser Phe Asp Ser Leu Phe Ser
            610                 615                 620

        Ala Val Lys Asn Phe Ser Glu Ala Ala Ser Asp Phe His Lys Arg Leu
        625                 630                 635                 640

25      Ile Gln Val Asp Leu Asn Asn Pro Ile Ala Val Arg Met Met Asn Asp
                        645                 650                 655

        Gln Leu Met Leu Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro
                    660                 665                 670

        Gly Lys Leu Phe Tyr Arg His Ile Ile Phe Ala Pro Ser Ser His Asn
30              675                 680                 685

        Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Ile Phe Asp
            690                 695                 700

        Ile Glu Asn Lys Ala Asn Ser Arg Leu Ala Trp Lys Glu Val Lys Lys
        705                 710                 715                 720

35      His Ile Ser Ile Ala Ala Phe Thr Ile Gln Ala Ala Ala Gly Thr Leu
                        725                 730                 735

        Lys Glu Val Leu
                    740


40      <210>   3
        <211>   20
        <212>   DNA
        <213>   artificial sequence
```

<220>
<223> forward primer

<400>   3
gccgtctgta cctttggatg   20

<210>   4
<211>   20
<212>   DNA
<213>   artificial sequence

<220>
<223>   reverse primer

<400>   4
agcccaccat aaatcccatc   20

<210>   5
<211>   22
<212>   DNA
<213>   artificial sequence

<220>
<223>   probe

<400>   5
ctgctgcgct ggcatctttc ct   22